

In the specification:

Please amend the specification as follows:

On page 1, before line 18, please **add** the following paragraph:

INCORPORATION OF SEQUENCE LISTING

A paper copy of the Sequence Listing and a computer readable form of the sequence listing on diskette, containing the file named 19006007.APP, which is 42,496 bytes in size (measured in WINDOWS XP), and which was created on January 27, 2006, are herein incorporated by reference.

Please **delete** the paragraph on page 15, lines 22-31 and **replace** it with the following paragraph:

With the process and kits according to the invention - with or without use of a nucleic acid amplification - a new method for pathogen detection is made available. As indicated in the following (Table 1 and Table II), for example the 16S rRNA of many pathogen species already naturally contains a 5'-~~GAAA~~-3' 5'-GAAA-3' ribozyme motif which can be used to form the hammerhead ribozyme. If the nucleic acids of the pathogens contain none of the sequence motifs suitable for the development of ribozymes, the former can, as indicated above, be introduced or "added" within the framework of the amplification stages by using suitable primers. (Table 1, 16S RNA region 70-100, SEQ ID NOS:44 and 53, respectively; region 115-145, SEQ ID NOS:19, 25, 54 and 83, respectively; region 145-175, SEQ ID NOS:20, 26, 32, 45, 55, 61, 71, 77, 84 and 90, respectively; region 180-210, SEQ ID NOS:33, 46, 62, 78 and 91, respectively; region 370-400, SEQ ID NOS:34, 47, 63, 72, 79 and 92, respectively; region 485-515, SEQ ID NOS:35, 64 and 93, respectively; region 595-625, SEQ ID NOS:21, 27, 36, 48, 56, 65, 73, 80, 85 and 94, respectively; region 625-655, SEQ ID NOS:28, 37, 57, 66, 81 and 95, respectively; region 650-680, SEQ ID NO:38; region 660-690, SEQ ID NOS:39, 67 and 74, respectively; region 685-715, SEQ ID NOS:22, 29, 40, 49, 58, 68, 75, 87 and 96, respectively; region 755-780, SEQ ID NOS:23, 30, 41, 50, 69, 76, 82, 88 and 97, respectively; region 895-925, SEQ ID NOS:42, 70 and 98, respectively; region 1000-1050, SEQ ID NO:51; region 1065-

1095, SEQ ID NOS:24, 31, 59 and 89, respectively; region 1245-1275, SEQ ID NOS:43 and 60, respectively; region 1305-1335, SEQ ID NO:52) (Table II, 16S RNA region 70-100, SEQ ID NO:127; region 115-145, SEQ ID NOS:19, 144, 151 and 181, respectively; region 145-175, SEQ ID NOS:32, 99, 111, 119, 128, 137, 20, 145, 152, 158, 163, 169, 175, 182, 190 and 196, respectively; region 180-210, SEQ ID NOS:33, 100, 129, 138, 159, 164, 170, 176 and 183, respectively; region 370-400, SEQ ID NOS:34, 101, 130, 165, 171, 177, 184 and 191, respectively; region 450-480, SEQ ID NOS:112, 120 and 139, respectively; region 485-515, SEQ ID NOS:35, 102, 113, 121 and 131, respectively; region 595-625, SEQ ID NOS:36, 103, 132, 140, 21, 146, 153, 160, 166, 172, 178, 185, 192 and 197, respectively; region 625-655, SEQ ID NOS:37, 104, 114, 122, 133, 147, 154 and 198, respectively; region 650-680, SEQ ID NOS:38 and 105, respectively; region 660-690, SEQ ID NOS:39 and 106, respectively; region 685-715, SEQ ID NOS:40, 107, 115, 123, 134, 141, 22, 148, 155, 161, 167, 173, 179, 186, 193 and 199, respectively; region 715-745, SEQ ID NOS:116 and 124, respectively; region 755-780, SEQ ID NOS:41, 108, 117, 125, 135, 142, 23, 149, 156, 162, 168, 174, 180, 187, 194 and 200, respectively; region 845-875, SEQ ID NO:143; region 895-925, SEQ ID NOS:42, 109, 118, 126, 136 and 201, respectively; region 1065-1095, SEQ ID NOS:24, 150, 157, 188 and 195, respectively; region 1245-1275, SEQ ID NOS:43, 110 and 189, respectively; region 1400-1430, SEQ ID NO:202)

Please **delete** Table 1 on pages 16-18, and **replace** it with the following Table:

Table 1: GAAA in 16S rRNA

Region in E. Coli 16S rNA	70-100	115-145
E. Coli	---	taatgtctgg GAAA actgcctgatg (SEQ ID NO: 19)
Salmonella	---	taatgtctgg GAAA actgcctgatg (SEQ ID NO: 25)
Staphylococcus	---	---
C. perfringens	tttccttcgg GAAA cggattagcg (SEQ ID NO: 44)	---
Vibrio	aagtcgagcg GAAA cgaattatct (SEQ ID NO: 53)	taatgcctag GAAA attgcctgat (SEQ ID NO: 54)
B. Cereus	---	---

C. botulinum	---	---
Campylobacter	---	---
Yersinia	---	taatgtctgg GAAA ctgcctgatg (SEQ ID NO: 83)
Listeria	---	---

Region in E. Coli 16S rNA	145-175	180-210
E. Coli	ataactactg GAAA cggtagctaa (SEQ ID NO: 20)	---
Salmonella	ataactactg GAAA cggtggctaa (SEQ ID NO: 26)	---
Staphylococcus	ataacttcgg GAAA cgggagctaa (SEQ ID NO: 32)	gttcaaaagt GAAA gacgggtcttg (SEQ ID NO: 33)
C. perfringens	atagccttcc GAAA ggaagattaa (SEQ ID NO: 45)	tcataatggt GAAA gatggcatca (SEQ ID NO: 46)
Vibrio	ataaccattg GAAA cgatggctaa (SEQ ID NO: 55)	---
B. Cereus	ataactccgg GAAA ccggggctaa (SEQ ID NO: 61)	cgcattggttc GAAA tt GAAA ggcg (SEQ ID NO: 62)
C. botulinum	atagccttcc GAAA ggaagattaa (SEQ ID NO: 71)	---
Campylobacter	acaacagttg GAAA cgactgctaa (SEQ ID NO: 77)	gttgagtagg GAAA gtttttcggt (SEQ ID NO: 78)
Yersinia	ataactactg GAAA cggtagctaa (SEQ ID NO: 84)	---
Listeria	ataactccgg GAAA ccggggctaa (SEQ ID NO: 90)	ccacgctttt GAAA gatgggttcg (SEQ ID NO: 91)

Region in E. Coli 16S rNA	370-400	485-515
E. Coli	---	---
Salmonella	---	---
Staphylococcus	cgcaatgggc GAAA gcctgacgga (SEQ ID NO: 34)	tacctaataca GAAA gccacggcta (SEQ ID NO: 35)
C. perfringens	agggtcattg GAAA ctg GAAA act (SEQ ID NO: 47)	---
Vibrio	---	---
B. Cereus	cgcaatggac GAAA gtctgacgga (SEQ ID NO: 63)	tacctaacca GAAA gccacggcta (SEQ ID NO: 64)
C. botulinum	cgcaatgggg GAAA ccctgacgga (SEQ ID NO: 72)	---
Campylobacter	cgcaatgggg GAAA ccctgacgca (SEQ ID NO: 79)	---
Yersinia	---	---
Listeria	cgcaatggac GAAA gtctgacgga (SEQ ID NO: 92)	tatctaacca GAAA gccacggcta (SEQ ID NO: 93)

Region in E. Coli 16S rNA	595-625	625-655
E. Coli	agtcagatgtGAAAtccccgggct (SEQ ID NO: 21)	---
Salmonella	agtcggatgtGAAAtccccgggct (SEQ ID NO: 27)	aactgcattcGAAActggcaggct (SEQ ID NO: 28)
Staphylococcus	agttctgatgtGAAAgcccacggct (SEQ ID NO: 36)	agggtcattgGAAActgGAAAct (SEQ ID NO: 37)
C. perfringens	agtgggatgtGAAAtaccgggct (SEQ ID NO: 48)	---
Vibrio	agtcagatgtGAAAgcccggggct (SEQ ID NO: 56)	nattgcatttGAAActggcagact (SEQ ID NO: 57)
B. Cereus	agttctgatgtGAAAgcccacggct (SEQ ID NO: 65)	agggtcattgGAAActgggagact (SEQ ID NO: 66)
C. botulinum	agtgggatgtGAAAtccccgggct (SEQ ID NO: 73)	---
Campylobacter	agttcttctgtGAAAtctaaggct (SEQ ID NO: 80)	aactgcttggGAAActgatagtct (SEQ ID NO: 81)
Yersinia	cagtcagatgtGAAAtccccgggct (SEQ ID NO: 85)	aactgcatttGAAActggcaagct (SEQ ID NO: 86)
Listeria	agttctgatgtGAAAgccccgggct (SEQ ID NO: 94)	agggtcattgGAAActggaagact (SEQ ID NO: 95)

Region in E. Coli 16S rNA	650-680	660-690
E. Coli	---	---
Salmonella	---	---
Staphylococcus	ttgGAAActgGAAActtgagtgc (SEQ ID NO: 38)	tgcagaagagGAAActggaattcc (SEQ ID NO: 39)
C. perfringens	---	---
Vibrio	---	---
B. Cereus	---	tgcagaagagGAAActggaattcc (SEQ ID NO: 67)
C. botulinum	---	tgcaggagagGAAAgcgggaattcc (SEQ ID NO: 74)
Campylobacter	---	---
Yersinia	---	---
Listeria	---	---

Region in E. Coli 16S rNA	685-715	755-780
E. Coli	gtgtagcgggtGAAAtgcgtagaga (SEQ ID NO: 22)	gctcaggtgcGAAAgcgtggggag (SEQ ID NO: 23)

Salmonella	gtgtagcgggGAAAtgcgtagaga (SEQ ID NO: 29)	gctcaggtgcGAAAgcgtggggag (SEQ ID NO: 30)
Staphylococcus	gtgtagcgggGAAAtgcgcagaga (SEQ ID NO: 40)	gctgatgtgcGAAAgcgtggggat (SEQ ID NO: 41)
C. perfringens	gtgtagcgggGAAAtgcgtagaga (SEQ ID NO: 49)	gctgaggctcGAAAgcgtggggag (SEQ ID NO: 50)
Vibrio	gtgtagcgggGAAAtgcgtagaga (SEQ ID NO: 58)	---
B. Cereus	gtgtagcgggGAAAtgcgtagaga (SEQ ID NO: 68)	actgaggcgcGAAAgcgtggggag (SEQ ID NO: 69)
C. botulinum	gtgtagcgggGAAAtgcgtagaga (SEQ ID NO: 75)	gctgaggcacGAAAgcgtgggtag (SEQ ID NO: 76)
Campylobacter	---	gctaaggcgcGAAAgcgtggggag (SEQ ID NO: 82)
Yersinia	gtgtagcgggGAAAtgcgtagaga (SEQ ID NO: 87)	gctcaggtgcGAAAgcgtggggag (SEQ ID NO: 88)
Listeria	gtgtagcgggGAAAtgcgtagata (SEQ ID NO: 96)	gctgaggcgcGAAAgcgtggggag (SEQ ID NO: 97)

Region in E. Coli 16S rNA	895-925	1000-1050
E. Coli	---	---
Salmonella	---	---
Staphylococcus	ccgcaagggtGAAActcaaaggaa (SEQ ID NO: 42)	---
C. perfringens	---	cttaatcgagGAAActccttcgggg (SEQ ID NO: 51)
Vibrio	---	---
B. Cereus	ccgcaagggtGAAActcaaaggaa (SEQ ID NO: 70)	---
C. botulinum	---	---
Campylobacter	---	---
Yersinia	---	---
Listeria	ccgcaagggtGAAActcaaaggaa (SEQ ID NO: 98)	---

Region in E. Coli 16S rNA	1065-1095	1245-1275
E. Coli	ctcgtgttgtGAAAtgttggtta (SEQ ID NO: 24)	---
Salmonella	ctcgtgttgtGAAAtgtcgggtta (SEQ ID NO: 31)	---
Staphylococcus	---	aaagggcagcGAAAccgcgaggtc (SEQ ID NO: 43)
C. perfringens	---	---

Vibrio	ctcgtgtttgt GAAA tgttgggtta (SEQ ID NO: 59)	gccaaacttgc GAAA gtgagcgaat (SEQ ID NO: 60)
B. Cereus	---	---
C. botulinum	---	---
Campylobacter	---	---
Yersinia	ctcgtgtttgt GAAA tgttgggtta (SEQ ID NO: 89)	---
Listeria	---	---

Region in E. Coli 16S rNA	1305-1335
E. Coli	---
Salmonella	---
Staphylococcus	---
C. perfringens	attgtaggct GAAA ctgcctaca (SEQ ID NO: 52)
Vibrio	---
B. Cereus	---
C. botulinum	---
Campylobacter	---
Yersinia	---
Listeria	---

Please **delete** Table II on pages 19-23, and **replace** it with the following Table:

Table II: GAAA in 16S rRNA

Region in E. coli 16S rRNA	70-100	115-145
S. aureus	---	---
S. epidermidis	---	---
S. pneumoniae	---	---
S. pyogenes	---	---
E. faecalis	cactcaattg GAAA gaggagtggc (SEQ ID NO: 127)	---
N. meningitides	---	---
E. coli	---	taatgtctgg GAAA ctgcctgatg (SEQ ID NO: 19)
Enterobacter spec.	---	taatgtctgg GAAA ctgccgatgg (SEQ ID NO: 144)
Proteus spec.	---	ggtaacagga GAAA gcttgctttc (SEQ ID NO: 151)
P. aeruginosa	---	---
P. fluorescens	---	---
P. mendocina	---	---

<i>P. syringae</i>	---	---
<i>H. influenzae</i>	---	ggtagcagga GAAA gcttgctttc (SEQ ID NO: 181)
<i>H. ducreyi</i>	---	---
<i>Bacteroides spec.</i>	---	---

Region in <i>E. coli</i> 16S rRNA	145-175	180-210
<i>S. aureus</i>	ataacttcgg GAAA ccggagctaa (SEQ ID NO: 32)	gttcaaaagt GAAA gacgggtcttg (SEQ ID NO: 33)
<i>S. epidermidis</i>	ataacttcgg GAAA ccggagctaa (SEQ ID NO: 99)	gttcaatagt GAAA gacgggttttg (SEQ ID NO: 100)
<i>S. pneumoniae</i>	ataactattg GAAA cgatagctaa (SEQ ID NO: 111)	---
<i>S. pyogenes</i>	ataactattg GAAA cgatagctaa (SEQ ID NO: 119)	---
<i>E. faecalis</i>	ataacacttg GAAA caggtgctaa (SEQ ID NO: 128)	gcataagagt GAAA ggcgctttcg (SEQ ID NO: 129)
<i>N. meningitides</i>	ataactgatc GAAA gatcagctaa (SEQ ID NO: 137)	tcttgagaga GAAA gcaggggacc (SEQ ID NO: 138)
<i>E. coli</i>	ataactactg GAAA cggtagctaa (SEQ ID NO: 20)	---
<i>Enterobacter spec.</i>	ataactactg GAAA cggtagctaa (SEQ ID NO: 145)	---
<i>Proteus spec.</i>	ataactactg GAAA cggtagctaa (SEQ ID NO: 152)	---
<i>P. aeruginosa</i>	ataacgtccg GAAA cggccgctaa (SEQ ID NO: 158)	tcctgaggg GAAA gtcggggatc (SEQ ID NO: 159)
<i>P. fluorescens</i>	ataacgttcg GAAA cggacgctaa (SEQ ID NO: 163)	tcctacggg GAAA gcaggggacc (SEQ ID NO: 164)
<i>P. mendocina</i>	ataacgttcc GAAA ggaacgctaa (SEQ ID NO: 169)	tcctacggg GAAA gcangggacc (SEQ ID NO: 170)
<i>P. syringae</i>	ataacgctcg GAAA cggacgctaa (SEQ ID NO: 175)	tcctacggg GAAA gcaggggacc (SEQ ID NO: 176)
<i>H. influenzae</i>	ataactactg GAAA cggtagctaa (SEQ ID NO: 182)	taaagggggc GAAA gctgttgcca (SEQ ID NO: 183)
<i>H. ducreyi</i>	ataactacgg GAAA ctgtagctaa (SEQ ID NO: 190)	---
<i>Bacteroides spec.</i>	atagcctttc GAAAGAAA gattaa (SEQ ID NO: 196)	---

Region in <i>E. coli</i> 16S rRNA	370-400	450-480
<i>S. aureus</i>	cgcaatgggc GAAA gcctgacgga (SEQ ID NO: 34)	---

S. epidermidis	cgcaatgggcGAAAgcctgacgga (SEQ ID NO: 101)	---
S. pneumoniae	---	tgtgagagtGAAAgttcacactg (SEQ ID NO: 112)
S. pyogenes	---	ggtgggagtGAAAtccaccaag (SEQ ID NO: 120)
E. faecalis	ggcaatggacGAAAgcttgaccga (SEQ ID NO: 130)	---
N. meningitides	---	tgtcagggaaGAAAggctgttgc (SEQ ID NO: 139)
E. coli	---	---
Enterobacter spec.	---	---
Proteus spec.	---	---
P. aeruginosa	---	---
P. fluorescens	gacaatgggcGAAAgcctgatcca (SEQ ID NO: 165)	---
P. mendocina	gacaatgggcGAAAgcctnatcca (SEQ ID NO: 171)	---
P. syringae	gacaatgggcGAAAgcctgatcca (SEQ ID NO: 177)	---
H. influenzae	cgcaatgggcGAAAccctgatgca (SEQ ID NO: 184)	---
H. ducreyi	cacaatgggcGAAAccctgatgca (SEQ ID NO: 191)	---
Bacteroides spec.	---	---

Region in E. coli 16S rRNA	485-515	595-625
S. aureus	tacctaatacGAAAgccacggcta (SEQ ID NO: 35)	agtctgatgtGAAAgccacggct (SEQ ID NO: 36)
S. epidermidis	tacctaatacGAAAgccacggcta (SEQ ID NO: 102)	agtctgatgtGAAAgccacggct (SEQ ID NO: 103)
S. pneumoniae	tatcttaccaGAAAgggacggcta (SEQ ID NO: 113)	---
S. pyogenes	taactaaccaGAAAgggacggcta (SEQ ID NO: 121)	---
E. faecalis	tatctaaccaGAAAgccacggcta (SEQ ID NO: 131)	agtctgatgtGAAAgccccggct (SEQ ID NO: 132)
N. meningitides	---	agcaggatgtGAAAtccccgggct (SEQ ID NO: 140)
E. coli	---	agtcagatgtGAAAtccccgggct (SEQ ID NO: 21)
Enterobacter spec.	---	aagtcgatgtGAAAtccccgggct (SEQ ID NO: 146)
Proteus spec.	---	agtcagatgtGAAAgccccgagct (SEQ ID NO: 153)

P. aeruginosa	---	agcttgatgt GAAA ccccgggct (SEQ ID NO: 160)
P. fluorescens	---	agttggatgt GAAA ccccgggct (SEQ ID NO: 166)
P. mendocina	---	agttggatgt GAAA gccccgggct (SEQ ID NO: 172)
P. syringae	---	agttgaatgt GAAA ccccgggct (SEQ ID NO: 178)
H. influenzae	---	agtgaggtgt GAAA gccctgggct (SEQ ID NO: 185)
H. ducreyi	---	agtgagatgt GAAA gccccgggct (SEQ ID NO: 192)
Bacteroides spec.	---	agtcagttgt GAAA gtttgcggt (SEQ ID NO: 197)

Region in E. coli 16S rRNA	625-655	650-680
S. aureus	agggtcattg GAAA ctg GAAA act (SEQ ID NO: 37)	ttg GAAA ctg GAAA acttgagtgc (SEQ ID NO: 38)
S. epidermidis	agggtcattg GAAA ctg GAAA act (SEQ ID NO: 104)	ttg GAAA ctg GAAA acttgagtgc (SEQ ID NO: 105)
S. pneumoniae	gtaggctttg GAAA ctgtttaact (SEQ ID NO: 114)	---
S. pyogenes	gtacgctttg GAAA ctggagaact (SEQ ID NO: 122)	---
E. faecalis	agggtcattg GAAA ctgggagact (SEQ ID NO: 133)	---
N. meningitides	---	---
E. coli	---	---
Enterobacter spec.	aactgcattg GAAA ctggcagctt (SEQ ID NO: 147)	---
Proteus spec.	aactgcattg GAAA ctggctggct (SEQ ID NO: 154)	---
P. aeruginosa	---	---
P. fluorescens	---	---
P. mendocina	---	---
P. syringae	---	---
H. influenzae	---	---
H. ducreyi	---	---
Bacteroides spec.	aattgcagtt GAAA ctggcagctt (SEQ ID NO: 198)	---

Region in E. coli 16S rRNA	660-690	685-715
S. aureus	tgcagaagag GAAA gtggaattcc (SEQ ID NO: 39)	gtgtagcgggt GAAA tgccgagaga (SEQ ID NO: 40)

S. epidermidis	tgcagaagag GAAA gtggaattcc (SEQ ID NO: 106)	gtgtagcgg GAAA tgcgcagaga (SEQ ID NO: 107)
S. pneumoniae	---	gtgtagcgg GAAA tgcgtagata (SEQ ID NO: 115)
S. pyogenes	---	gtgtagcgg GAAA tgcgtagata (SEQ ID NO: 123)
E. faecalis	---	gtgtagcgg GAAA tgcgtagata (SEQ ID NO: 134)
N. meningitides	---	gtgtagcag GAAA tgcgtagaga (SEQ ID NO: 141)
E. coli	---	gtgtagcgg GAAA tgcgtagaga (SEQ ID NO: 22)
Enterobacter spec.	---	gtgtagcgg GAAA tgcgtagaga (SEQ ID NO: 148)
Proteus spec.	---	gtgtagcgg GAAA tgcgtagaga (SEQ ID NO: 155)
P. aeruginosa	---	gtgtagcgg GAAA tgcgtagata (SEQ ID NO: 161)
P. fluorescens	---	gtgtagygg GAAA tgcgttgata (SEQ ID NO: 167)
P. mendocina	---	gtgtagcgg GAAA tgcgtagata (SEQ ID NO: 173)
P. syringae	---	gtgtagcgg GAAA tgcgtagata (SEQ ID NO: 179)
H. influenzae	---	gtgtagcgg GAAA tgcgtagaga (SEQ ID NO: 186)
H. ducreyi	---	gtgtagcgg GAAA tgcgtagaga (SEQ ID NO: 193)
Bacteroides spec.	---	gtgtagcgg GAAA tgccttagata (SEQ ID NO: 199)

Region in E. coli 16S rRNA	715-745	755-780
S. aureus	---	gctgatgtgc GAAA gcgtggggat (SEQ ID NO: 41)
S. epidermidis	---	gctgatgtgc GAAA gcgtggggat (SEQ ID NO: 108)
S. pneumoniae	caccggtggc GAAA gcggctctct (SEQ ID NO: 116)	gctgaggctc GAAA gcgtggggag (SEQ ID NO: 117)
S. pyogenes	caccggtggc GAAA gcggctctct (SEQ ID NO: 124)	gctgaggctc GAAA gcgtggggag (SEQ ID NO: 125)
E. faecalis	---	gctgaggctc GAAA gcgtggggag (SEQ ID NO: 135)
N. meningitides	---	gttcattgccc GAAA gcgtgggtag (SEQ ID NO: 142)
E. coli	---	gctcaggtgc GAAA gcgtggggag (SEQ ID NO: 23)

Enterobacter spec.	---	gctcaggtgc GAAA gcgtggggag (SEQ ID NO: 149)
Proteus spec.	---	gctcaggtgc GAAA gcgtggggag (SEQ ID NO: 156)
P. aeruginosa	---	actgaggtgc GAAA gcgtggggag (SEQ ID NO: 162)
P. fluorescens	---	actgaggtgc GAAA gcgtggggag (SEQ ID NO: 168)
P. mendocina	---	actgaggtgc GAAA gcgtggggag (SEQ ID NO: 174)
P. syringae	---	actgaggtgc GAAA gcgtggggag (SEQ ID NO: 180)
H. influenzae	---	gctcatgtgt GAAA gcgtggggag (SEQ ID NO: 187)
H. ducreyi	---	gctcatgtgt GAAA gcgtggggag (SEQ ID NO: 194)
Bacteroides spec.	---	actgatgctc GAAA gtgtgggtat (SEQ ID NO: 200)

Region in E. coli 16S rRNA	845-475	895-925
S. aureus	---	ccgcaaggtt GAAA actcaaaggaa (SEQ ID NO: 42)
S. epidermidis	---	ccgcaaggtt GAAA actcaaaggaa (SEQ ID NO: 109)
S. pneumoniae	---	ccgcaaggtt GAAA actcaaaggaa (SEQ ID NO: 118)
S. pyogenes	---	ccgcaaggtt GAAA actcaaaggaa (SEQ ID NO: 126)
E. faecalis	---	ccgcaaggtt GAAA actcaaaggaa (SEQ ID NO: 136)
N. meningitides	gctaacgcgt GAAA ttgaccgcct (SEQ ID NO: 143)	---
E. coli	---	---
Enterobacter spec.	---	---
Proteus spec.	---	---
P. aeruginosa	---	---
P. fluorescens	---	---
P. mendocina	---	---
P. syringae	---	---
H. influenzae	---	---
H. ducreyi	---	---
Bacteroides spec.	---	cggcaacggt GAAA actcaaaggaa (SEQ ID NO: 201)

Region in E. coli 16S rRNA	1065-1095	1245-1275
S. aureus	---	aaagggcagc GAAA ccgcgaggtc (SEQ ID NO: 43)
S. epidermidis	---	aaagggtagc GAAA ccgcgaggtc (SEQ ID NO: 110)
S. pneumoniae	---	---
S. pyogenes	---	---
E. faecalis	---	---
N. meningitides	---	---
E. coli	ctcgtgttgt GAAA tgttgggtta (SEQ ID NO: 24)	---
Enterobacter spec.	ctcgtgttgt GAAA tgttgggtta (SEQ ID NO: 150)	---
Proteus spec.	tcgttgttgt GAAA tgttgggtta (SEQ ID NO: 157)	---
P. aeruginosa	---	---
P. fluorescens	---	---
P. mendocina	---	---
P. syringae	---	---
H. influenzae	ctcgtgttgt GAAA tgttgggttn (SEQ ID NO: 188)	gcgaatctca GAAA gtgcatctaa (SEQ ID NO: 189)
H. ducreyi	ctcgtgttgt GAAA tgttgggttn (SEQ ID NO: 195)	---
Bacteroides spec.	---	---

Region in E. coli 16S rRNA	1400-1430
S. aureus	---
S. epidermidis	---
S. pneumoniae	---
S. pyogenes	---
E. faecalis	---
N. meningitides	---
E. coli	---
Enterobacter spec.	---
Proteus spec.	---
P. aeruginosa	---
P. fluorescens	---
P. mendocina	---
P. syringae	---
H. influenzae	---
H. ducreyi	---
Bacteroides spec.	gaataacgtg GAAA catgttagcc (SEQ ID NO: 202)

Please **delete** the paragraph on page 24, lines 19-28, and **replace** it with the following paragraph:

Fig. 2. A: General structure of hammerhead ribozymes (SEQ ID NOS 208 and 209). Only preserved nucleotides are identified by corresponding letters, all non-preserved positions are shown as N. The length of the hybridizing arms can be adjusted to the requirements in each case. Three locations for possible hairpin loops are shown by dotted lines. The polarity (5'-3' direction) is given only for the cleaved section. B: (SEQ ID NOS 208 and 209) Corresponds to Fig. 2A, the positions at which the ribonucleotides are preferably used being provided with the prefix "r", while the remaining nucleotides can in each case be either ribo- or deoxyribonucleotides.

Please **delete** the paragraph on page 24, lines 30-32, and **replace** it with the following paragraph:

Fig. 3: A possibility for cleaving a minimal ribozyme and a nucleic acid substrate probe (SEQ ID NOS 208 and 210). The preserved ribozyme motif was shortened to GAAA (SEQ ID NO: 1).

Please **delete** the paragraph on page 25, lines 2-9, and **replace** it with the following paragraph:

Fig. 4: A: Based on the possibility shown in Fig. 3, an amplified nucleic acid (thick line) is shown with the minimal ribozyme motif (SEQ ID NO: 208). The nucleic acid substrate probe contains reporters and quenchers (a few possibilities are given below) at both ends (SEQ ID NO: 211), but they can also be linked to other positions. B: (SEQ ID NOS 208 and 212) Corresponds to Fig. 4A, the positions at which ribonucleotides are preferably placed are

provided with the prefix “r”, while the remaining nucleotides can in each case be either ribo- or deoxyribonucleotides.

Please **delete** the paragraph on page 25, lines 11-13, and **replace** it with the following paragraph:

Fig. 5: A further possibility for cleaving a nucleic acid substrate probe (SEQ ID NO: 213). The preserved ribozyme motif (SEQ ID NO: 209) is reduced to CUGA-N-GA (SEQ ID NO: 2).

Please **delete** the paragraph on page 25, lines 15-19, and **replace** it with the following paragraph:

Fig. 6: Based on the possibility shown in Fig. 5, an amplified nucleic acid (think line) is shown with the minimal ribozyme motif (SEQ ID NO: 209). The nucleic acid substrate probe (SEQ ID NO: 214) contains reporters and quenchers at both ends, but they can also be linked to other positions (cf. Fig. 4).

Please **delete** the paragraph on page 25, lines 21-26, and **replace** it with the following paragraph:

Fig. 7: Based on the possibility shown in Fig. 3, the reverse primer (SEQ ID NO: 215) contains the ribozyme motif. The hybrid between primary target nucleic acid and primer is shown above. The position within the target nucleic acid and the length of the base-pair-forming section can vary. The resulting amplified nucleic acid with the complete ribozyme motif is shown below (SEQ ID NO: 208).

Please **delete** the paragraph on page 25, lines 28-33, and **replace** it with the following paragraph:

Fig. 8: Based on the possibility shown in Fig. 3, the reverse primer (SEQ ID NO: 215) contains the ribzyme motif in a bulge. The hybrid between primary target nucleic acid and primer is shown above. The position within the target nucleic acid and the length of both base-pair-forming sections can vary. The resulting amplified nucleic acid with the complete ribzyme motif is shown below (SEQ ID NO: 208).

Please **delete** the paragraph on page 26, lines 2-10, and **replace** it with the following paragraph:

Fig. 9: Based on the possibility shown in Fig. 3, the reverse primer contains the ribzyme motif in a bulge, followed by a very short 3'-terminal base-paired section. As is shown, this section can overlap with the ribzyme motif and the bulge can be so short that it comprises only one nucleotide. The hybrid between primary target nucleic acid and primer is shown above. The position within the target nucleic acid and the length of both base-pair-forming sections can vary. The resulting amplified nucleic acid with the complete ribzyme motif is shown below (SEQ ID NO: 208).

Please **delete** the paragraph on page 26, lines 12-18, and **replace** it with the following paragraph:

Fig. 10: Based on the possibility shown in Fig. 2B, the reverse primer contains the ribzyme motif in a bulge followed by a single rA-T base pairing with the target sequence. The hybrid between primary target nucleic acid and primer is shown above. The position within the target nucleic acid and the length of both base-pair-forming sections can vary. The resulting amplified nucleic acid with the complete ribzyme motif is shown below (SEQ ID NO: 216).

Please **delete** the paragraph on page 26, lines 20-22, and **replace** it with the following paragraph:

Fig. 11: Corresponds to the possibility shown in Fig. 10. Here, however, the target sequence already contains a longer stretch of the ribozyme motif (or, as shown, of the complete motif) **(above: SEQ ID NO: 217, below: SEQ ID NO: 216).**

Please **delete** the paragraph on page 26, lines 24-26, and **replace** it with the following paragraph:

Fig. 12: By way of example, structure of a DNAzyme(=catalytic DNA) **(SEQ ID NO: 218).** The substrate can either be wholly RNA, or a minimum of rA must be present.

Please **delete** the paragraph on page 26, lines 28-30, and **replace** it with the following paragraph:

Fig. 13: By way of example, structure of another DNAzyme **(SEQ ID NO: 219).** The substrate can either be wholly RNA, or a minimum of rRrY must be present.

Please **delete** the paragraph on page 27, lines 2-8, and **replace** it with the following paragraph:

Fig. 14: Corresponds to Fig. 10, the primer containing the greatest part of the Nazyme motif (of the catalytic nucleic acid motif) and only the two last nucleotides being absent **(SEQ ID NOS 220 and 221).** Shown here is a possibility based on “prototype A”. For “prototype B”, the presence of longer motifs (e.g. TCGTTG instead of TCGT) makes it possible to use a more

deleted motif in the primer, the 3'-terminal ACGA in the elongated primer **(SEQ ID NO: 222)** being supplied by the target sequence.

Please **delete** the paragraph on page 27, line 10, and **replace** it with the following paragraph:

Fig. 15: Example of a universal ribozyme probe **(left: SEQ ID NO: 5, right: SEQ ID NO: 206)**.

Please **delete** the paragraph on page 27, line 12, and **replace** it with the following paragraph:

Fig. 16: Example of a HIV ribozyme probe **(left: SEQ ID NO: 7, right: SEQ ID NO: 223)**.

Please **delete** the paragraph on page 28, lines 14-35, and **replace** it with the following paragraph:

Experiment A:

(dNTP = upper case letters: rNTP = lower case letters)

Primer 1: 5'- AAT TCT AAT ACG ACT CAC TAT AGG GTG CTA TGT CAC TTC CCC
TTG GTT CTC TCA-3' **(SEQ ID NO: 9)**

Primer 2: 5'- GAA TCT CAT CAG TAG CGA GTG GGG GGA CAT CAA GCA GCC
ATG CAA A-3' **(SEQ ID NO: 10)**

Substrate A: 5'- TAMRA-Tga auc gaa acg cga aag cgu cua gcg u-FAM-3' **(SEQ ID NO: 11)**

Experiment B:

Primer 1: 5'- AAT TCT AAT ACG ACT CAC TAT AGG GTG CTA TGT CAC TTC CCC
TTG GTT CTC TCA-3' **(SEQ ID NO: 9)**

Primer 2: 5'- ACG TAG TTT CGG CCT TTC GGC CTC ATC AGC GTG CAG TGG
GGG GAC ATC AAG CAG CCA TGC AAA-3' **(SEQ ID NO: 203)**

Substrate B: 5'-TAMRA-Tac gua guc cgu gcu-FAM-3' **(SEQ ID NO: 13)**

Please **delete** the paragraph on page 30, lines 1-13, and **replace** it with the following paragraph:

At its 3' end, the reverse primer contains the usual target-specific sequence (N) and in addition at its 5' end a sequence which codes for the general universal ribozyme motif:

5'-GCG TTT CGA TTC CNN NNN N... **(SEQ ID NO: 204)**

The transcript ends with the sequence

5'-...N NNN NNG GAA UCG AAA CGC **(SEQ ID NO: 205)**

The ribozyme probe contained the following sequence:

5'-GCG UC - U AGC GGA AAC GCU ACU GAX GAG AUU CC (32-mer) **(SEQ ID NO: 206)**

- cleavage site

Two dyes 5'-Q and 3'-R (or 3'-Q and 5'-R) were linked to the ends.

Please **delete** the paragraph on page 31, line 22, to page 32, line 4, and **replace** it with the following paragraph:

Amplified segment of the HIV-RNA:

agtggggggacatcaagcagctatgcaaa (c,t) gttaaaagatactatcaatgaggaagctgcagaat
gggacaggggtacatccagttacatgcagggcctattccaccaggccagatgagagaaccaaggggaagtg
acatagca (SEQ ID NO: 15)

(only one strand is shown, the primer sequences are underlined). The proximal sequence is likewise highly preserved and includes the following section:

agcagctatgGaaa (c,t) gttaaaaga (SEQ ID NO: 16)

The forward primer for the introduction of the T7 promoter sequence (upper case letters) and 1 point mutation (bold upper case letters):

AATTCTAATACGACTCACTATAGGGagtggggggacatcaagcagctatgGaaa
(SEQ ID NO: 17)

The transcript product contains the GAAA ribozyme motif which is linked to the proximal HIV-specific sequence:

GGGagcagctatgGaaa (c,t) gttaaaaga . . . (SEQ ID NO: 207)